

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2002, 18:48:48 ; Search time 1490.17 Seconds
(without alignments)
1217.774 Million cell updates/sec

Title: US-09-486-094-1

Perfect score: 110

Sequence: 1 aggtcggtgcaggcagat.....gaacgtgtcgacggatccgg 110

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 824859755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_om.*

20: em_or.*

21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pl.*

25: em_ro.*

26: em_sts.*

27: em_sy.*

28: em_un.*

29: em_vi.*

30: em_htgo_hum.*

31: em_htgo_inv.*

32: em_htgo_rod.*

33: em_htg_hum.*

34: em_htg_inv.*

35: em_htg_rod.*

36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	110	100.0	110	6	A98893	A98893 Sequence 1
2	110	100.0	211	6	A98895	A98895 Sequence 3
C 3	97	88.2	97	6	A98899	A98899 Sequence 7
C 4	44	40.0	44	6	A98898	A98898 Sequence 6
C 5	35	31.8	87	6	A95931	A95931 Sequence 9
C 6	35	31.8	98	6	A95925	A95925 Sequence 3
C 7	34	30.9	109	6	AX014753	AX014753 Sequence
C 8	34	30.9	169	6	AX014747	AX014747 Sequence
C 9	34	30.9	261	6	AX014748	AX014748 Sequence
C 10	33	30.7	261	6	A95927	A95927 Sequence 5
C 11	31.6	28.7	1430	14	AF086568	AF086568 Human ade
C 12	31.6	28.7	1430	14	AF086569	AF086569 Human ade
C 13	30.6	27.8	10344	1	AE008178	AE008178 Agrobacte
C 14	30.2	27.5	148975	2	AC012145	AC012145 Homo sapi
C 15	30.2	27.5	246240	6	AR036572	AR036572 Sequence
C 16	30.2	27.5	246240	6	AR036573	AR036573 Sequence
C 17	30.2	27.5	246240	6	AR036574	AR036574 Sequence
C 18	30.2	27.5	246282	9	HSU91328	U91328 Human hered
C 19	30	27.3	165432	9	AL512590	AL512590 Human DNA
C 20	30	27.3	178647	2	AL449464	AL449464 Homo sapi
C 21	29.8	27.1	119657	2	AC073667	AC073667 Mus muscu
C 22	29.8	27.1	170139	2	AC073727	AC073727 Mus muscu
C 23	29.6	26.9	178803	2	AC032028	AC032028 Homo sapi
C 24	29.6	26.9	209832	2	AP001891	AP001891 Homo sapi
C 25	29.4	26.7	219522	2	AC091324	AC091324 Mus muscu
C 26	29.2	26.5	38962	1	SC2E1	AL023797 Streptomy
C 27	29.2	26.5	183634	2	AC023167	AC023167 Mus muscu
C 28	29	26.4	134011	2	AC068269	AC068269 Homo sapi
C 29	29	26.4	168979	2	AC027451	AC027451 Homo sapi
C 30	28.8	26.2	228856	2	AC087420	AC087420 Mus muscu
C 31	28.6	26.0	134	11	G43892	G43892 WIAF-3511-S
C 32	28.6	26.0	37017	3	U12366	U12366 Caenorhabdi
C 33	28.6	26.0	159941	2	AC006878	AC006878 Caenorhab
C 34	28.4	25.8	1290	14	AF086571	AF086571 Human ade
C 35	28.4	25.8	1317	14	AF086567	AF086567 Human ade
C 36	28.4	25.8	35100	14	AF108105	AF108105 Human ade
C 37	28.4	25.8	110375	2	AC010572	AC010572 Drosophil
C 38	28.4	25.8	122624	2	AC015158	AC015158 Drosophil
C 39	28.4	25.8	150408	2	AC079902	AC079902 Homo sapi
C 40	28.4	25.8	166067	3	AC008325	AC008325 Drosophil
C 41	28.4	25.8	184444	2	AC025065	AC025065 Homo sapi
C 42	28.4	25.8	185648	9	AC006210	AC006210 Homo sapi
C 43	28.4	25.8	254808	3	AE003609	AE003609 Drosophil
C 44	28.2	25.6	2721	10	MUSSV40	M33654 SV40/Mouse
C 45	28.2	25.6	11436	2	AC014191	AC014191 Drosophil

ALIGNMENTS

RESULT 1
A98893 A98893 Sequence 1 110 bp DNA PAT 26-JAN-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

unidentified.
unidentified.
unclassified.
1 (bases 1 to 110)
Derose,R. and Hoffmann,J.
GENE CODING FOR ANDROCTONINE, VECTOR CONTAINING SAME AND
TRANSFORMED DISEASE-RESISTANT PLANTS OBTAINED
Patent: WO 9909189-A 1 25-FEB-1999;
DEROSE RICHARD (FR); HOFFMANN JULES (FR)
Location/Qualifiers
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/db_xref="taxon:32644"

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/translation="RSVCRQIKICRRRGCGYYKCTNRPY"
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QY 61 actaacaggccactagctcggcgaggcggaacgtgtcgacggtatccgg 110
Db 61 ACTAACAGGCCACTAGCTCGGCGGAGGCGAAGCTGTGACGGATCCGG 110

RESULT 2
A98895
LOCUS A98895 211 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 3 from Patent WO9909189.
ACCESSION A98895
VERSION A98895.1 GI:6781856
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 211)
AUTHORS Derose,R. and Hoffmann,J.
TITLE GENE CODING FOR ANDROCTONINE, VECTOR CONTAINING SAME AND
TRANSFORMED DISEASE-RESISTANT PLANTS OBTAINED
JOURNAL Patent: WO 9909189-A 3 25-FEB-1999;
DEROSE RICHARD (FR); HOFFMANN JULES (FR)
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12..179
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GCYYKCTNRPY"
BASE COUNT      33 a   58 c   57 g   63 t
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Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 aggtccgtgtgcaggcagatcaagatctgcaggagaggggtgtgtctactacaagtgc 60
Db 102 AGGTCCGTGTGCAGGCAGATCAAGATCTGCAGGAGGAGGGGTGTGTCTACTACAAGTGC 161

QY 61 actaacaggccactagctcggcgaggcggaacgtgtcgacggtatccgg 110
Db 162 ACTAACAGGCCACTAGCTCGGCGGAGGCGAAGCTGTGACGGATCCGG 211

RESULT 3
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LOCUS A98899 97 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 7 from Patent WO9909189.
ACCESSION A98899
VERSION A98899.1 GI:6781861
KEYWORDS
SOURCE
ORGANISM
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KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 97)
AUTHORS Derose,R. and Hoffmann,J.
TITLE GENE CODING FOR ANDROCTONINE, VECTOR CONTAINING SAME AND
TRANSFORMED DISEASE-RESISTANT PLANTS OBTAINED
JOURNAL Patent: WO 9909189-A 7 25-FEB-1999;
DEROSE RICHARD (FR); HOFFMANN JULES (FR)
FEATURES
Location/Qualifiers
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BASE COUNT      16 a   35 c   22 g   24 t
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Best Local Similarity 100.0%; Score 97; DB 6; Length 97;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ggcagatcaagatctgcaggagaggggtgtgtctactacaagtgcactaacaggccat 73
Db 97 GGCAGATCAAGATCTGCAGGAGGAGGGGTGTGTCTACTACAAGTGCACIACACAGCCAT 38

QY 74 actgagctcggcgaggcggaacgtgtcgacggtatccgg 110
Db 37 ACTGAGCTCGGCGAGGCGGAACGTGTGACGGATCCGG 1

RESULT 4
A98898
LOCUS A98898 44 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 6 from Patent WO9909189.
ACCESSION A98898
VERSION A98898.1 GI:6781860
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 44)
AUTHORS Derose,R. and Hoffmann,J.
TITLE GENE CODING FOR ANDROCTONINE, VECTOR CONTAINING SAME AND
TRANSFORMED DISEASE-RESISTANT PLANTS OBTAINED
JOURNAL Patent: WO 9909189-A 6 25-FEB-1999;
DEROSE RICHARD (FR); HOFFMANN JULES (FR)
FEATURES
Location/Qualifiers
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Db 1 AGGTCCGTGTGCAGGCAGATCAAGATCTGCAGGAGGAGGGGTGTGTCTACTACAAGTGC 44

RESULT 5
A95931/c
LOCUS A95931 87 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 9 from Patent WO9924594.
ACCESSION A95931
VERSION A95931.1 GI:6779839
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
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unclassified.
REFERENCE
AUTHORS      Derose,R. and Hoffmann,J.
TITLE        GENE CODING FOR THIANATIN, VECTOR CONTAINING SAME AND RESULTING
JOURNAL      TRANSFORMED DISEASE-RESISTANT PLANTS
              Patent: WO 9924594-A 9 20-MAY-1999;
              DEROSE RICHARD (FR); HOFFMANN JULES (FR)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 tgaactcgcgcgagcgacacgtgtcgacgacatccg 110
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Db 35 TGAGCTCGCGAGGCGACGACGTGTGCGACGGATCCG 1

RESULT 6
A95925 LOCUS AX014753 109 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 8 from Patent WO9953053.
ACCESSION AX014753
VERSION A95925.1 GI:10041022
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequence.

REFERENCE
AUTHORS      Derose,R. and Hoffmann,J.
TITLE        GENE CODING FOR THIANATIN, VECTOR CONTAINING SAME AND RESULTING
JOURNAL      TRANSFORMED DISEASE-RESISTANT PLANTS
              Patent: WO 9924594-A 3 20-MAY-1999;
              DEROSE RICHARD (FR); HOFFMANN JULES (FR)
FEATURES
source       1..98
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              /db_xref="GI:6779831"
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BASE COUNT   25 a 23 c 34 g 16 t
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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 tgaactcgcgcgagcgacacgtgtcgacgacatccg 110
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Db 64 TGAGCTCGCGAGGCGACGACGTGTGCGACGGATCCG 98

RESULT 7
AX014753/c LOCUS AX014753 109 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 8 from Patent WO9953053.
ACCESSION AX014753
VERSION A95925.1 GI:10041022
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    artificial sequence.

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REFERENCE
AUTHORS      Lamberty,M., Hofmann,J., Bulet,P. and Brookhart,G.L.
TITLE        Gene coding for heliomicine and use thereof
JOURNAL      Patent: WO 9953053-A 8 21-OCT-1999;
              LAMBERTY MIRILLE (FR); HOFMANN JULES (FR); BULET PHILIPPE (FR);
              RHONE POULENC AGROCHIMIE (FR); BROOKHART GARY LEE (US)
FEATURES
source       1..109
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Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 gagctcgcgcgagcgacacgtgtcgacgacatccg 110
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Db 34 GAGCTCGCGAGGCGACGACGTGTGCGACGGATCCG 1

RESULT 8
AX014747 LOCUS AX014747 169 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9953053.
ACCESSION AX014747
VERSION AX014747.1 GI:10041013
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.
              artificial sequence.

REFERENCE
AUTHORS      Lamberty,M., Hofmann,J., Bulet,P. and Brookhart,G.L.
TITLE        Gene coding for heliomicine and use thereof
JOURNAL      Patent: WO 9953053-A 2 21-OCT-1999;
              LAMBERTY MIRILLE (FR); HOFMANN JULES (FR); BULET PHILIPPE (FR);
              RHONE POULENC AGROCHIMIE (FR); BROOKHART GARY LEE (US)
FEATURES
source       1..169
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BASE COUNT   33 a 36 c 61 g 39 t
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Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 gagctcgcgcgagcgacacgtgtcgacgacatccg 110
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Db 136 GAGCTCGCGAGGCGACGACGTGTGCGACGGATCCG 169

RESULT 9
AX014748 LOCUS AX014748 261 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 3 from Patent WO9953053.
ACCESSION AX014748
VERSION AX014748.1 GI:10041015
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct.

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artificial sequence.
1 (bases 1 to 261)
AUTHORS Lamberty,M., Hofmann,J., Bulet,P. and Brookhart,G.L.
TITLE Gene coding for heliomicine and use thereof
JOURNAL Patent: WO 9953053-A 3 21-OCT-1999;
LAMBERTY MIREILLE (FR); HOFMANN JULES (FR); BULET PHILIPPE (FR);
RHONE POULENC AGROCHIMIE (FR); BROOKHART GARY LEE (US)
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BASE COUNT 39 a 66 c 74 g 82 t
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Query Match 30.9%; Score 34; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 77 gagctggcggcgaacgtgtcgacgagatccgg 110
Db 228 GAGCTCGCGGAGCGAACGTGTGCGACGGATCCG 261

RESULT 10
A95927
LOCUS A95927 197 bp DNA PAT 26-JAN-2000
DEFINITION Sequence 5 from patent WO9924594.
ACCESSION A95927
VERSION A95927.1 GI:6779834
KEYWORDS
SOURCE
    ORGANISM
        unidentified.
        unclassified.
        unclassified.
REFERENCE 1 (bases 1 to 197)
AUTHORS Derose,R. and Hoffmann,J.
TITLE GENE CODING FOR THANATIN, VECTOR CONTAINING SAME AND RESULTING
TRANSFORMED DISEASE-RESISTANT PLANTS
JOURNAL Patent: WO 9924594-A 5 20-MAY-1999;
DEROSE RICHARD (FR); HOFFMANN JULES (FR)
FEATURES
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    /db_xref="GI:6779835"
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    TGKQCRM"
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Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 tgagctggcggcgaacgtgtcgacgagatcc 108
Db 165 TGAGCTCGCGGAGCGAACGTGTGCGACGGATCC 197

RESULT 11

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AF086568/c
LOCUS AF086568 1430 bp DNA VRL 01-NOV-2000
DEFINITION Human adenovirus type 19 early E3B 10.4 kDa protein, early E3B 14.5
kDa protein, and early E3B 14.7 kDa protein genes, complete cds.
ACCESSION AF086568
VERSION AF086568.1 GI:6940694
KEYWORDS
    SOURCE      Human adenovirus type 19.
    ORGANISM    Human adenovirus type 19.
REFERENCE 1 (bases 1 to 1430)
AUTHORS Blusch,J.H. and Burgert,H.-G.
TITLE Immunomodulatory functions encoded by the E3 transcription unit of
adenoviruses
JOURNAL Virus Genes 21 (1-2), 13-25 (2000)
MEDLINE 20475623
PUBMED 11022786
REFERENCE 2 (bases 1 to 1430)
AUTHORS Blusch,J.H. and Burgert,H.-G.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1998) Virology, Max-von-Pettenkofer-Institute,
Feodor Lynen Str. 25, Munich 81377, Germany
FEATURES
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    /db_xref="taxon:28278"
    /note="number 86858 as described by Wadell,G. and de
    Jong,J.C. Infectio. Immun., 27, 292-296, 1980
    subtype: Ad19a"
    1..276
    /codon_start=1
    /product="early E3B 10.4 kDa protein"
    /protein_id="AAF31741.1"
    /db_xref="GI:6940695"
    /translation="MIPRFLNIFLCENICAAFAAVSHASPDCLGPPPTYLLFALL
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    279..671
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    /protein_id="AAF31742.1"
    /db_xref="GI:6940696"
    /translation="MOTLLMLLSLPALATYADYSKCKFADIMNFLDCYQEKIDMPS
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    FFLQYLEPEPPPPSTVSVFHTGDD"
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    /db_xref="GI:6940697"
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    IHCSCEPICYSLKLTCLGLRLLPMN"
BASE COUNT 328 a 474 c 275 g 353 t
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Best Local Similarity 56.9%; Pred. No. 4.8;
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 8 tqtgcaggcagatcaagatctgcaggaggagggtgtgtctactacaagtgcactaaca 67
Db 651 TGTGAAGACTAGCTAACAGTGGAGGGGTCTCTTAAGTACTGTATCA 592

Qy 68 ggcctactagctgcggcaggcgaacgtgtcgacgagatccg 109
Db 591 GGGGAAGCTGTTCTCGGAGGAGCGGTGTGGTGTGGCG 550

RESULT 12
AF086569/c
LOCUS AF086569 1430 bp DNA VRL 01-NOV-2000
DEFINITION Human adenovirus type 37 early E3B 10.4 kDa protein, early E3B 14.5

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Accession AF086569.1 GI:6940700
Version AF086569.1
Keywords
Source
Organism
Human adenovirus type 37.
Human adenovirus type 37
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
Reference 1 (bases 1 to 1430)
Burgert, H.G. and Blusch, J.H.
Immunomodulatory functions encoded by the E3 transcription unit of adenoviruses
Virus Genes 21 (1-2), 13-25 (2000)
Medline 20475623
Pubmed 11022786
Reference 2 (bases 1 to 1430)
Blusch, J.H. and Burgert, H.-G.
Direct Submission
Title Submitted (25-AUG-1998) Virology, Max-von-Pettenkofer-Institute, Feodor Lynen Str. 25, Munich 81377, Germany
Journal
Features
source
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/organism="Human adenovirus type 37"
/strain="G.W.; ATCC VR-929"
/db_xref="taxon:38437"
/db_xref="ATCC:VR-929"
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/protein_id="AAF31744.1"
/db_xref="GI:6940701"
/translation="MTPREFLEILFLCNICAAFAVSHASPDCLGPFPTLLFALL
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279. .671
/codon_start=1
/product="early E3B 14.5 kDa protein"
/protein_id="AAF31745.1"
/db_xref="GI:6940702"
/translation="MQTLLMLLSLPALATYADYSKCKFADINFLDCYQEKIDMPS
YFLVTVGVVWCSTCFAMIFPCFDLGNVSVEAFYTLSSSLASTPPTPPRRNQ
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/db_xref="GI:6940703"
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IKCSCEPCLYSLKYLGLRLDPNN"
BASE COUNT 328 a 474 c 275 g 353 t
ORIGIN
Query Match 28.7%; Score 31.6; DB 14; Length 1430;
Best Local Similarity 56.9%; Pred. No. 4.8;
Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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RESULT 13
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LOCUS
DEFINITION Agrobacterium tumefaciens strain C58 circular chromosome, section 236 of 254 of the complete sequence.
ACCESSION AE008178
VERSION AE008178.1
KEYWORDS

Source ORGANISM Agrobacterium tumefaciens.
Agrobacterium tumefaciens
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
REFERENCE 1 (bases 1 to 10344)
Hinkle, G., Slater, S.C. and Goodner, B.
Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall
Disease in Plants
Unpublished
REFERENCE 2 (bases 1 to 10344)
Hinkle, G., Slater, S.C. and Goodner, B.
Direct Submission
Title Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
Cambridge, MA 02139, USA
Journal
Features
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